

SCORE Search Results Details for Application 10573229 and Search Result 20090528_121103_us-10-573-229a-1.mi.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
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This page gives you Search Results detail for the Application 10573229 and Search Result 20090528_121103_us-10-573-229a-1.mi.

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GenCore version 6.3

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OM nucleic - nucleic search, using sw model

Run on: May 31, 2009, 22:10:23 ; Search time 1097 Seconds
(without alignments)
5968.836 Million cell updates/sec

Title: US-10-573-229A-1
Perfect score: 920
Sequence: 1 tctgtagaggggaatggctg.....acccccaaagaaaccttcta 920

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9875436 seqs, 3558593875 residues

Total number of hits satisfying chosen parameters: 19750872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /ABSS/Data/CRF/ptodata/1/ina/1_COMB.seq:*
- 2: /ABSS/Data/CRF/ptodata/1/ina/5_COMB.seq:*
- 3: /ABSS/Data/CRF/ptodata/1/ina/6A_COMB.seq:*
- 4: /ABSS/Data/CRF/ptodata/1/ina/6B_COMB.seq:*
- 5: /ABSS/Data/CRF/ptodata/1/ina/7A_COMB.seq:*
- 6: /ABSS/Data/CRF/ptodata/1/ina/7B_COMB.seq:*
- 7: /ABSS/Data/CRF/ptodata/1/ina/7C_COMB.seq:*
- 8: /ABSS/Data/CRF/ptodata/1/ina/7D_COMB.seq:*
- 9: /ABSS/Data/CRF/ptodata/1/ina/HA_COMB.seq:*
- 10: /ABSS/Data/CRF/ptodata/1/ina/HB_COMB.seq:*
- 11: /ABSS/Data/CRF/ptodata/1/ina/PCTUS_COMB.seq:*
- 12: /ABSS/Data/CRF/ptodata/1/ina/PP_COMB.seq:*
- 13: /ABSS/Data/CRF/ptodata/1/ina/RE_COMB.seq:*
- 14: /ABSS/Data/CRF/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Query Match	Length	DB	ID	
	1	322.2	35.0	650	9	US-09-925-065A-602935	Sequence 602935,
	2	309.8	33.7	501	9	US-09-925-065A-602938	Sequence 602938,
	3	149.6	16.3	485	9	US-09-925-065A-425353	Sequence 425353,
	4	122.6	13.3	561	3	US-09-573-080A-108	Sequence 108, App
	5	122.6	13.3	561	5	US-09-854-867-108	Sequence 108, App
	6	121.2	13.2	541	3	US-09-573-080A-107	Sequence 107, App
	7	121.2	13.2	541	5	US-09-854-867-107	Sequence 107, App
c	8	119.6	13.0	493	9	US-09-925-065A-176178	Sequence 176178,
c	9	119.6	13.0	504	10	US-10-301-480C-643499	Sequence 643499,
c	10	109.6	11.9	590	9	US-09-925-065A-73587	Sequence 73587, A
c	11	109.6	11.9	590	9	US-09-925-065A-73588	Sequence 73588, A
c	12	109.6	11.9	590	10	US-10-301-480C-550895	Sequence 550895,
c	13	109.6	11.9	590	10	US-10-301-480C-550896	Sequence 550896,
	14	104.8	11.4	737	7	US-10-105-299-6677	Sequence 6677, Ap
	15	104.8	11.4	797	7	US-10-105-299-234	Sequence 234, App
c	16	104.8	11.4	137000	3	US-10-172-911-11	Sequence 11, Appl
c	17	98.4	10.7	84105	6	US-10-741-601-5637	Sequence 5637, Ap
c	18	98	10.7	55927	3	US-09-949-016-15017	Sequence 15017, A
c	19	97.8	10.6	9245	3	US-09-949-016-13349	Sequence 13349, A
c	20	97.8	10.6	9245	3	US-09-949-016-13350	Sequence 13350, A
	21	93	10.1	948	10	US-10-301-480C-92013	Sequence 92013, A
c	22	91.8	10.0	143550	3	US-09-949-016-14143	Sequence 14143, A
	23	91.2	9.9	992	10	US-10-301-480C-220057	Sequence 220057,
	24	90.8	9.9	76118	3	US-09-949-016-15593	Sequence 15593, A
	25	90.4	9.8	806	10	US-10-301-480C-325534	Sequence 325534,
	26	90.2	9.8	564	9	US-09-925-065A-236350	Sequence 236350,
	27	90.2	9.8	574	10	US-10-301-480C-695058	Sequence 695058,
	28	89.4	9.7	589	10	US-10-301-480C-427272	Sequence 427272,
	29	89.4	9.7	589	10	US-10-301-480C-427274	Sequence 427274,
	30	89.4	9.7	589	10	US-10-301-480C-605967	Sequence 605967,
	31	89.4	9.7	592	9	US-09-925-065A-134131	Sequence 134131,
	32	89	9.7	589	10	US-10-301-480C-427273	Sequence 427273,
	33	88.4	9.6	987	10	US-10-301-480C-932619	Sequence 932619,
c	34	86.6	9.4	660	10	US-10-301-480C-296865	Sequence 296865,
c	35	85.4	9.3	870	10	US-10-301-480C-296866	Sequence 296866,
	36	85.2	9.3	463	9	US-09-925-065A-594086	Sequence 594086,
	37	85.2	9.3	575	9	US-09-925-065A-333372	Sequence 333372,
	38	85.2	9.3	577	10	US-10-301-480C-783034	Sequence 783034,
	39	85.2	9.3	986	10	US-10-301-480C-163837	Sequence 163837,
	40	85.2	9.3	987	10	US-10-301-480C-950354	Sequence 950354,
	41	85.2	9.3	987	10	US-10-301-480C-950355	Sequence 950355,
	42	84.8	9.2	915	8	US-10-098-754-678	Sequence 678, App
	43	84.2	9.2	997	10	US-10-301-480C-326425	Sequence 326425,
	44	84.2	9.2	55927	3	US-09-949-016-15017	Sequence 15017, A
c	45	84	9.1	601	3	US-09-949-016-178228	Sequence 178228,

ALIGNMENTS

RESULT 1

US-09-925-065A-602935
; Sequence 602935, Application US/09925065A
; Patent No. H002191
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 602935
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-602935

Query Match		35.0%;	Score 322.2;	DB 9;	Length 650;		
Best Local Similarity		95.4%;	Pred. No. 1.2e-93;				
Matches	354;	Conservative	0;	Mismatches	13;	Indels	4; Gaps 2;
Qy	373	GCTGGGCGACTGAGAAGCATCACCCACTTCCCCAGAACCTTTTTTTACGTGGAGTGAAAAC	432				
Db	1	GCTGGGCGACTGAGAAGCATCACCCACTTCCCCAGAACCTTTTTTTACGTGGAGTGAAAAC	60				
Qy	433	TTTAAGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAATTTCTCTGCTTC	492				
Db	61	TTTAAGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAATTTCTCTGCTTC	120				
Qy	493	TGCAAAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTAAAACCCTCCCTG	552				
Db	121	TGCAAAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTAAAACCCTCCCTG	180				
Qy	553	CCCCAGGCCCAAGCAAGGATTTCCCTAGCGGGGAGGAAGGTAGAATCGAGAGACCTCTA	612				
Db	181	CCCCAGGCCCAAGCAAGGATTTCCCTAGCGGGGAGGAAGGTAGAATCGAGAGACCTCTA	240				
Qy	613	ACCCTGGGAGAGGAGGGAGGGAAATCTCCGAGGACCAGGGTTATGCAACAACACAAGGGA	672				
Db	241	ACCCTGGGAGAGGAGGGAGGGAAATCTCCGAGGACCAGGGTTATGCAACAACACAAGGGA	300				
Qy	673	AGTACCTGCTGGGTTCTGGGGGTTGGGGAAGGAAAATCCCTACTGCCCCAAGAGCCAGCC	732				

Db 301 AGTACCTGCTGG---TTCTGGGGTTGGGGAGGAAGATCCCTACTG-CCCAAGAGCCAGCA 356

Qy 733 CCGAACCCAAG 743

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Db 357 CAGACACAAGG 367

RESULT 2

US-09-925-065A-602938

; Sequence 602938, Application US/09925065A

; Patent No. H002191

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single

; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.135

; CURRENT APPLICATION NUMBER: US/09/925,065A

; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 60/243,096

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250,092

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/289,846

; PRIOR FILING DATE: 2001-05-09

; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 602938

; LENGTH: 501

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-925-065A-602938

Query Match 33.7%; Score 309.8; DB 9; Length 501;

Best Local Similarity 94.5%; Pred. No. 1.1e-89;

Matches 343; Conservative 0; Mismatches 17; Indels 3; Gaps 2;

Qy 381 ACTGAGAAGCATCACCCACTTCCCCAGAACCTTTTTTACGTGGAGTGAAAACCTTTAAGGG 440

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Db 1 ACTGAGAAGCATCACCCACTTCCCCAGAGCCTTTTTTACATGGAGTGAAAACCTTTAAGGG 60

Qy 441 GCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAATTTCTCTGCTTCTGCAAAAAG 500

|||||

Db 61 GCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAAGTTCTCTGCTTCTGCAAAAAG 120

Qy 501 GACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTAAAACCTCCCTGCCCCAGGC 560

|||||

Db 121 GACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTAAAACCTCCCTGCCCCAGGC 180

Qy 561 CCCAAGCAAGGATTTCCCTAGCGGGGAGGAAGGTAGAATCGAGAGACCTCTAACCCCTGGG 620

|||||

Db 181 CCCAAGCAAGGATTTCCCTAGCGGGGAGGAAGGTAGAATCGAAAGACCTCTAACCCCTGGG 240

Qy 621 AGAGGAGGGAGGGGAAATCTCCGAGGACCAGGGTTATGCAACAACACAAGGGAAGTACCTG 680

```

                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          241 AGAGGAGGGAGGGAAATCTCCGAGGACCAGGGTTATGCAACAACACAAGGGAAGTACCTG 300

Qy          681 CTGGGTTCTGGGGGTTGGGGAAGGAAAATCCCTACTGCCCCAAGAGCCAGCCCCGAACCC 740
                ||||  |  ||||  ||  ||||  |||||||||  |||||||||  ||  |  |
Db          301 CTGG--TTCTGGGGTCAGGGGAGGAAGATCCCTACTG-CCCAAGAGCCAGCACAGACACA 357

Qy          741 AAG 743
                |  |
Db          358 AGG 360
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RESULT 3

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US-09-925-065A-425353
; Sequence 425353, Application US/09925065A
; Patent No. H002191
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 425353
; LENGTH: 485
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-425353
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Query Match          16.3%; Score 149.6; DB 9; Length 485;
Best Local Similarity 91.0%; Pred. No. 1.5e-37;
Matches 193; Conservative 0; Mismatches 14; Indels 5; Gaps 3;
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```

Qy          532 ACGGGGGTAAACCTCCCTGCCCCAGGCCCAAGCAAGGATTTCCCTAGCGGGGAGGAA 591
                |||||||||||||||  |||||||||||||||||||||||||||||||||||
Db          1  ACGGGGGTAAACCTTCCCTGCCCCAGGCCCAAGCAAGGATTTCCCTAGCGGGGAGGAA 60

Qy          592 GGTAGAATCGAGAGACCTCTAACCTGGGAGAGGAGGGAGGGAAAATCTCCGAGGACCAGG 651
                |||||||||||||||  |||||||||||||||||||||||||||||||
Db          61 GGTAGAATCGAGAGACCTCTAA-CCTGGGAGAGGAGGGAGGGAAAATCTCCGAGGACCAGG 119

Qy          652 GTTATGCAACAACACAAGGGAAGTACCTGCTGGGTTCTGGGGGTTGGGGAAGGAAAATCC 711
                |||||||||||||||  |||||||||||  |||  |||  ||||  ||||
Db          120 GTTATGCAACAACACAAGGGAAGTACCTGCTGG---TTCTGGGGTGGGGAGGAAGATCC 176
```

Qy 712 CTACTGCCCCAAGAGCCAGCCCCGAACCCAAG 743
| | | | | | | | | | | | | | | | | | | | |
Db 177 CTACTG-CCCAAGAGCCAGCACAGACACAAGG 207

RESULT 4

US-09-573-080A-108
; Sequence 108, Application US/09573080A
; Patent No. 6828097
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOLL
; APPLICANT: ROGAN, PETER
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING SAME
; FILE REFERENCE: 30307
; CURRENT APPLICATION NUMBER: US/09/573,080A
; CURRENT FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 108
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: (1)..(561)
; OTHER INFORMATION: mlt1f1
; NAME/KEY: misc_feature
; OTHER INFORMATION: n is a, c, g or t
; PUBLICATION INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A
; TITLE: Prototypic sequences for human repetitive DNA
; JOURNAL: Journal of Molecular Evolution
; VOLUME: 35
; ISSUE: 4
; PAGES: 286-291
; DATE: 1992-10-__
; DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase)
; DATABASE ENTRY DATE: ____-__-__
; DATABASE ENTRY DATE: 1996-01-26
US-09-573-080A-108

Query Match 13.3%; Score 122.6; DB 3; Length 561;
Best Local Similarity 69.6%; Pred. No. 1e-28;
Matches 201; Conservative 0; Mismatches 74; Indels 14; Gaps 2;

Qy 2 CTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGC 61
| | | | | | | | | | | | | | | | | | | | |
Db 201 CTCTGGGGGAAGCCAGCTGCCATGTCATGAGGACACTCAAGCAGCCCTGTGGAGAGGCC 260

Qy 62 ACTTGGTGAGAAACCGATGCCT-CTGCCAACCCACCTGCACTAACCTGCTGGGTC----- 114
| | | | | | | | | | | | | | | | | | | | |
Db 261 ATGTGGCAAGGAAGTGGCCTCCTGCCAACAGCCAGCAAGGAAGTGGCCTCCTGCCA 320

Qy 115 -----TGAGACTGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGC 167
| | | | | | | | | | | | | | | | | | | | |

```
Db          321 ACAGCCATGTGAGTGAGCCATCTTGGAAGCAGATCCTCCAGCCCCAGTCAAGCCTTCAGA 380
Qy          168 TGGCTGCAGCCACAGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATC 227
          || ||||| |||| |||| | ||||| |||| | || ||||| |||| |
Db          381 TGACTGCAGCCCCAGCTAACATCTTGACTGCAACCTCATGAGAGACCCTGAGCCAGAACC 440
Qy          228 CCCTGGCTAAATTGCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA 276
          || |||| | |||| | |||| | |||| | |||| | ||
Db          441 ACCCAGCTAAGCTGCTCCTAAATTCTGACCCACAGAACTGTGAGAGA 489
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RESULT 5

US-09-854-867-108

; Sequence 108, Application US/09854867

; Patent No. 7014997

; GENERAL INFORMATION:

; APPLICANT: JOAN, KNOLL H

; APPLICANT: ROGAN, PETER K

; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING SAME

; FILE REFERENCE: 30307

; CURRENT APPLICATION NUMBER: US/09/854,867

; CURRENT FILING DATE: 2003-05-08

; NUMBER OF SEQ ID NOS: 613

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 108

; LENGTH: 561

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: repeat_region

; LOCATION: (1)..(561)

; OTHER INFORMATION: mlt1f1

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (62)..(62)

; OTHER INFORMATION: n is a, c, g or t

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (165)..(165)

; OTHER INFORMATION: n is a, c, g or t

US-09-854-867-108

Query Match 13.3%; Score 122.6; DB 5; Length 561;

Best Local Similarity 69.6%; Pred. No. 1e-28;

Matches 201; Conservative 0; Mismatches 74; Indels 14; Gaps 2;

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Qy          2 CTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGC 61
          || || || || |||| | |||| | |||| | |||| | ||
Db          201 CTCTGGGGGAAGCCAGCTGCCATGTCATGAGGACACTCAAGCAGCCCTGTGGAGAGGCC 260
Qy          62 ACTTGGTGAGAAACCGATGCCT-CTGCCAACCCACCTGCACTAACCTGCTGGGTC----- 114
          | ||| || ||| || |||| | |||| | ||| | ||
Db          261 ATGTGGCAAGGAAGTGGCCTCCTGCCAACAGCCAGCAAGGAAGTGGCCTCCTGCCA 320
Qy          115 -----TGAGACTGAGCCACTTTGGAAGCTGATCTTGAGCACCAGTCAAGCCCTTAGC 167
          || || ||||| ||||| |||| | ||| ||||| |||| | ||
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```
Db          321 ACAGCCATGTGAGTGAGCCATCTTGGAAGCAGATCCTCCAGCCCCAGTCAAGCCTTCAGA 380
Qy          168 TGGCTGCAGCCACAGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATC 227
          || ||||| |||| |||| | ||||| |||| | || ||||| |||| |
Db          381 TGACTGCAGCCCCAGCTAACATCTTGACTGCAACCTCATGAGAGACCCTGAGCCAGAACC 440
Qy          228 CCCTGGCTAAATTGCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA 276
          || ||||| ||||| |||| | ||||| |||| |||| |||
Db          441 ACCCAGCTAAGCTGCTCCTAAATTCTGACCCACAGAACTGTGAGAGA 489
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RESULT 6

US-09-573-080A-107

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; Sequence 107, Application US/09573080A
; Patent No. 6828097
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOLL
; APPLICANT: ROGAN, PETER
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
SAME
; FILE REFERENCE: 30307
; CURRENT APPLICATION NUMBER: US/09/573,080A
; CURRENT FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 107
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: (1)..(541)
; OTHER INFORMATION: mltlf
; NAME/KEY: misc_feature
; OTHER INFORMATION: n is a, c, g or t
; PUBLICATION INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A
; TITLE: Prototypic sequences for human repetitive DNA
; JOURNAL: Journal of Molecular Evolution
; VOLUME: 35
; ISSUE: 4
; PAGES: 286-291
; DATE: 1992-10-__
; DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase)
; DATABASE ENTRY DATE: ____-__-__
; DATABASE ENTRY DATE: 1996-01-26
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US-09-573-080A-107

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Query Match          13.2%; Score 121.2; DB 3; Length 541;
Best Local Similarity 68.8%; Pred. No. 2.8e-28;
Matches 190; Conservative 3; Mismatches 81; Indels 2; Gaps 2;
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Qy          2 CTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGC 61
          || || || || |||| || ||| | | ||||| | ||||| || |
Db          197 CTCTGGGGGAAGCCAGCTGCCATGCTATGAAGACACTCAAGCAGCCTA-TGAGAGAAGTCC 255
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Qy          62 ACTTGGTGAGAAACCGATGCCT-CTGCCAACACCTGCACTAACCTGCTGGGTCTGAGAC 120
    || |||  || ||| || | || ||||| || ||  ||:||| |  || ||
Db          256 ACGTGGSAAAGGAAGTCTCCTGCCAACAGCCAGCTTCGACYTGCCAGCCATGTGAG 315

Qy          121 TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC 180
    ||||| ||||| |||| | ||| |||||:|||| | || || ||||| ||
Db          316 TGAGCCATCTTGGAAGCGGATCCTCCAGCCCCAGTYAAGCCTTCAGATGACTGCAGCCCC 375

Qy          181 AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT 240
    || ||| | ||||| ||||| || | || ||||| ||||| || ||||| |
Db          376 GGCTGACATCTTGACTGCAACCTCATGAGAGACCCTGAGCCAGAACTACCCAGCTAAGCT 435

Qy          241 GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA 276
    ||||| :|||| | ||||| ||||| |||| | |
Db          436 GCTCCTARATTCCTGACCCACAGAACTGTGAGATA 471
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RESULT 7

US-09-854-867-107

; Sequence 107, Application US/09854867

; Patent No. 7014997

; GENERAL INFORMATION:

; APPLICANT: JOAN, KNOLL H

; APPLICANT: ROGAN, PETER K

; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING SAME

; FILE REFERENCE: 30307

; CURRENT APPLICATION NUMBER: US/09/854,867

; CURRENT FILING DATE: 2003-05-08

; NUMBER OF SEQ ID NOS: 613

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 107

; LENGTH: 541

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: repeat_region

; LOCATION: (1)..(541)

; OTHER INFORMATION: mlt1f

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (179)..(179)

; OTHER INFORMATION: n is a, c, g or t

US-09-854-867-107

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Query Match          13.2%;  Score 121.2;  DB 5;  Length 541;
Best Local Similarity 68.8%;  Pred. No. 2.8e-28;
Matches 190;  Conservative 3;  Mismatches 81;  Indels 2;  Gaps 2;
```

```
Qy          2 CTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGC 61
    || | | ||  |||| | || || |  |  ||||| | ||||| || |
Db          197 CTCTGGGGGAAGCCAGCTGCCATGCTATGAAGACACTCAAGCAGCCTA-TGAGAAAGTCC 255

Qy          62 ACTTGGTGAGAAACCGATGCCT-CTGCCAACACCTGCACTAACCTGCTGGGTCTGAGAC 120
    || |||  || ||| || | || ||||| || ||  ||:||| |  || ||
Db          256 ACGTGGSAAAGGAAGTCTCCTGCCAACAGCCAGCTTCGACYTGCCAGCCATGTGAG 315
```

```
Qy      121 TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC 180
      ||||| ||||| ||| | ||| ||||:|||| | || || ||||| |
Db      316 TGAGCCATCTTGGAAGCGGATCCTCCAGCCCCAGTYAAGCCTTCAGATGACTGCAGCCCC 375

Qy      181 AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT 240
      || ||| | ||||| ||||| || | || ||||| ||||| || ||||| |
Db      376 GGCTGACATCTTGACTGCAACCTCATGAGAGACCCTGAGCCAGAACTACCCAGCTAAGCT 435

Qy      241 GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA 276
      ||||| :|||| | ||||| |||| | || |
Db      436 GCTCCTARATTCTTGACCCACAGAACTGTGAGATA 471
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RESULT 8

US-09-925-065A-176178/c

; Sequence 176178, Application US/09925065A

; Patent No. H002191

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single

; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.135

; CURRENT APPLICATION NUMBER: US/09/925,065A

; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 60/243,096

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250,092

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/289,846

; PRIOR FILING DATE: 2001-05-09

; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 176178

; LENGTH: 493

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-925-065A-176178

Query Match 13.0%; Score 119.6; DB 9; Length 493;
Best Local Similarity 66.7%; Pred. No. 9e-28;
Matches 184; Conservative 1; Mismatches 90; Indels 1; Gaps 1;

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Qy      2 CTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGC 61
      || | |||| ||||| ||||| ||| | | ||||| || ||||| |
Db      419 CTCTGGAGGAAGTCAGCTGCTGTGTCATGAGGGCACTCAAACAGCCCTATGAAGAGGTCC 360

Qy      62 ACTTGGTGAGAAACCGATGCC-TCTGCCAACCCACCTGCACTAACCTGCTGGGTCTGAGAC 120
      | |||| || ||| || | | ||||| || ||| |||| ||| ||| || ||
Db      359 ATGTGGTAAGGAAGTGAAGTCTGCTGCCAACAGCCAGCAATAACTTGCCAGGTATGTGAA 300

Qy      121 TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC 180
      || |||| ||||| || | | | |||| |||| || | ||| ||| |
Db      299 TGTGCCATCTTGGAAGCAAGTTCTCCAACCTCCAGACAAGCTCTCTAATAACTGTGGCCCC 240
```

```
Qy      181 AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT 240
      ||| ||| | | ||||| | | ||| ||||| | | || |:|||
Db      239 AGCTGACATCTTGGCTGCAACCCACGAGGGAATCTGAGCCAGCACCACCAAGMTAAGCC 180

Qy      241 GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA 276
      |||| | || | |||| |||| | |
Db      179 ACTCCTAAATTCCTGACTTGCAGAAAATGTGTGAAA 144
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RESULT 9

US-10-301-480C-643499/c

; Sequence 643499, Application US/10301480C

; Patent No. H002220

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single

; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

; FILE REFERENCE: 108827-137

; CURRENT APPLICATION NUMBER: US/10/301,480C

; CURRENT FILING DATE: 2002-11-21

; PRIOR APPLICATION NUMBER: US 10/215,598

; PRIOR FILING DATE: 2002-08-09

; PRIOR APPLICATION NUMBER: US 60/311,695

; PRIOR FILING DATE: 2001-08-10

; NUMBER OF SEQ ID NOS: 989478

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 643499

; LENGTH: 504

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-301-480C-643499

```
Query Match          13.0%;  Score 119.6;  DB 10;  Length 504;
Best Local Similarity 66.7%;  Pred. No. 9.1e-28;
Matches 184;  Conservative 1;  Mismatches 90;  Indels 1;  Gaps 1;
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```
Qy      2 CTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGC 61
      || | |||| | ||||| ||||| ||| | | ||||| || ||||| |
Db      430 CTCTGGAGGAAGTCAGCTGCTGTGTCATGAGGGCACTCAAACAGCCCTATGAAGAGGTCC 371

Qy      62 ACTTGGTGAGAAACCGATGCC-TCTGCCAACCACTGCACTAACCTGCTGGGTCTGAGAC 120
      | |||| || ||| || | | ||||| || ||| |||| ||| ||| || ||
Db      370 ATGTGGTAAGGAAGTGAAGGACTTCTGCCAACAGCCAGCAATAACTTGCCAGGTATGTGAA 311

Qy      121 TGAGCCACTTTGGAAGCTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC 180
      || |||| ||||| | | | |||| |||| | ||| ||| |
Db      310 TGTGCCATCTTGGAAGCAAGTTCTCCAACCCAGACAAGCTCTCTAATAACTGTGGCCCC 251

Qy      181 AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT 240
      ||| ||| | | ||||| | | ||| ||||| | | || |:|||
Db      250 AGCTGACATCTTGGCTGCAACCCACGAGGGAATCTGAGCCAGCACCACCAAGMTAAGCC 191

Qy      241 GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA 276
      |||| | || | |||| |||| | |
Db      190 ACTCCTAAATTCCTGACTTGCAGAAAATGTGTGAAA 155
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RESULT 10

US-09-925-065A-73587/c
; Sequence 73587, Application US/09925065A
; Patent No. H002191
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73587
; LENGTH: 590
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-73587

Query Match 11.9%; Score 109.6; DB 9; Length 590;
Best Local Similarity 63.8%; Pred. No. 1.8e-24;
Matches 166; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

Qy	17	GCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGCACTTGGTGAGAAACC	76
Db	299	GCTTCCATGTCATGAGGATATTCCAGCAATTCTATTAAGAGTCCACATGGCAAGGAACTG	240
Qy	77	GATGCCTCTGCCAACCACTGCACTAACCTGCTGGGTCTGAGACTGAGCCACTTTGGAAG	136
Db	239	AGGTCTTCTGCCAACCAACAGCATTAAACATTCCAGGCTTGTGGGTGAGTCCCTTTGGAAG	180
Qy	137	CTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCACAGCCAACAACAAGACT	196
Db	179	CAGATCCTCCAGACTCAGTCAAGCCATCAGATGACTGCAGTCCCAGGTGATGCCCAAGCT	120
Qy	197	GCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATTGCTCCTTGATTCTTAA	256
Db	119	GCAACCTCAAGAAAGATCCTGAGCCAGAACCACTCAGCTAAGTAGCTCTCAGGTTCTCTGA	60
Qy	257	CCCACAGAAATTGTGTAAGA	276
Db	59	CCTACAGCAACTGTGTGAGA	40

RESULT 11

US-09-925-065A-73588/c

; Sequence 73588, Application US/09925065A
; Patent No. H002191
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73588
; LENGTH: 590
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-73588

Query Match 11.9%; Score 109.6; DB 9; Length 590;
Best Local Similarity 63.8%; Pred. No. 1.8e-24;
Matches 166; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

Qy 17 GCTGCTGTGTCATGGGGGTGCATGAGCAGCCAGTGGAGAGGTGCACTTGGTGAGAAACC 76
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 299 GCTTCCATGTCATGAGGATATTCCAGCAATTCTATTAAGAGTCCACATGGCAAGGAAGT 240

Qy 77 GATGCCTCTGCCAACCACTGCACTAACCTGCTGGGTCTGAGACTGAGCCACTTTGGAAG 136
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 239 AGGTCTTCTGCCAACCAACAGCATTAAACATTCCAGGCTTGTGGGTGAGTCCCTTTGGAAG 180

Qy 137 CTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCACAGCCAACAACAAGACT 196
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 179 CAGATCCTCCAGACTCAGTCAAGCCATCAGATGACTGCAGTCCCAGGTGATGCCCAAGCT 120

Qy 197 GCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATTGCTCCTTGATTCTTAA 256
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 119 GCAACCTCAAGAAAGATCCTGAGCCAGAACCACTCAGCTAAGTAGCTCTCAGGTTCTGA 60

Qy 257 CCCACAGAAATTGTGTGAAGA 276
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 59 CCTACAGCAACTGTGTGAGA 40

RESULT 12
US-10-301-480C-550895/c
; Sequence 550895, Application US/10301480C
; Patent No. H002220
; GENERAL INFORMATION:

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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827-137
; CURRENT APPLICATION NUMBER: US/10/301,480C
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 989478
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 550895
; LENGTH: 590
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480C-550895
```

Query Match 11.9%; Score 109.6; DB 10; Length 590;
Best Local Similarity 63.8%; Pred. No. 1.8e-24;
Matches 166; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

Qy	17	GCTGCTGTGTTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGCACTTGGTGAGAAACC	76
Db	299	GCTTCCATGTCATGAGGATATTCCAGCAATTCTATTAAGAGTCCACATGGCAAGGAACTG	240
Qy	77	GATGCCTCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGACTGAGCCACTTTGGAAG	136
Db	239	AGGTCTTCTGCCAACAACCAGCATTAAACATTCCAGGCTTGTGGGTGAGTCCCTTTGGAAG	180
Qy	137	CTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCACAGCCAACAACAAGACT	196
Db	179	CAGATCCTCCAGACTCAGTCAAGCCATCAGATGACTGCAGTCCCAGGTGATGCCCCAAGCT	120
Qy	197	GCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATTGCTCCTTGATTCTTAA	256
Db	119	GCAACCTCAAGAAAGATCCTGAGCCAGAACCACTCAGCTAAGTAGCTCTCAGGTTCTGA	60
Qy	257	CCCACAGAAATTGTGTAAGA	276
Db	59	CCTACAGCAACTGTGTGAGA	40

RESULT 13

US-10-301-480C-550896/c

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; Sequence 550896, Application US/10301480C
; Patent No. H002220
; GENERAL INFORMATION:
;   APPLICANT: Wang, David G.
;   TITLE OF INVENTION: Identification and Mapping of Single
;   TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
;   FILE REFERENCE: 108827-137
;   CURRENT APPLICATION NUMBER: US/10/301,480C
;   CURRENT FILING DATE: 2002-11-21
;   PRIOR APPLICATION NUMBER: US 10/215,598
;   PRIOR FILING DATE: 2002-08-09
;   PRIOR APPLICATION NUMBER: US 60/311,695
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; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 989478
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 550896
; LENGTH: 590
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480C-550896

Query Match 11.9%; Score 109.6; DB 10; Length 590;
Best Local Similarity 63.8%; Pred. No. 1.8e-24;
Matches 166; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

Qy 17 GCTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGCACTTGGTGAGAAACC 76
||| | ||||| || | ||| | | ||| | | |||
Db 299 GCTTCCATGTCATGAGGATATTCCAGCAATTCTATTAAGAGTCCACATGGCAAGGAACTG 240

Qy 77 GATGCCTCTGCCAACCACTGCACTAACCTGCTGGGTCTGAGACTGAGCCACTTTGGAAG 136
| ||||| ||| ||| ||| | | || | ||| | |||||
Db 239 AGGTCTTCTGCCAACCAACAGCATTAACTCCAGGCTTGTGGGTGAGTCCCTTTGGAAG 180

Qy 137 CTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCACAGCCAACAACAAGACT 196
| |||| | || ||||| ||| || ||||| | ||| | | |||
Db 179 CAGATCCTCCAGACTCAGTCAAGCCATCAGATGACTGCAGTCCCAGGTGATGCCCAAGCT 120

Qy 197 GCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATTGCTCCTTGATTCTTAA 256
|||||| | ||||| ||||| | | |||| | |||| | ||| | |
Db 119 GCAACCTCAAGAAAGATCCTGAGCCAGAACCACTCAGCTAAGTAGCTCTCAGGTTCTGA 60

Qy 257 CCCACAGAAATTGTGTGAAGA 276
|| |||| || |||| |||
Db 59 CCTACAGCAACTGTGTGAGA 40

RESULT 14

US-10-105-299-6677
; Sequence 6677, Application US/10105299
; Patent No. 7368527
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6677
; LENGTH: 737
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-299-6677

Query Match 11.4%; Score 104.8; DB 7; Length 737;
Best Local Similarity 68.5%; Pred. No. 7.3e-23;
Matches 174; Conservative 0; Mismatches 77; Indels 3; Gaps 2;

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Qy      24  TGTTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGCACTTGGTGAGAAACCGATGCCT  83
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      398  TTTCATGAGGATACTCAAGCATTCCCTATGGAGAGATCCACATGGTGAGAAACTGAAGCCT  457

Qy      84  -CTGCCAACCACTGCACTAACCTGCTGGGTCTGAGACTGAGCCACTTTGGAAGCTGATC  142
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      458  CCTACCAAGAGCCAGCACCAACTTGCCAGCTATGTGAATGAGCCATCTTAGAAGTGGGT  517

Qy     143  TTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCACAGCCAACAACAAGACTGCAACC  202
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     518  CTCTAGCCCTAGTCAGGCCTTCATATGACTGCAGCCAGGGCTGATATTTTGACTACAACC  577

Qy     203  TCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATTGCTCCTTGATTCTTAACCCACA  262
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     578  TCATGAGAGA--CTGAGCCACAACAACCTAGCTAAGAAGCTCCTGAATCCCTACCAACA  635

Qy     263  GAAATTGTGTAAGA 276
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     636  GAAACTATGTGAGA 649
```

RESULT 15

US-10-105-299-234

```
; Sequence 234, Application US/10105299
; Patent No. 7368527
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 234
; LENGTH: 797
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-299-234
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Query Match          11.4%; Score 104.8; DB 7; Length 797;
Best Local Similarity 68.5%; Pred. No. 7.7e-23;
Matches 174; Conservative 0; Mismatches 77; Indels 3; Gaps 2;
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```
Qy      24  TGTTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGCACTTGGTGAGAAACCGATGCCT  83
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      383  TTTCATGAGGATACTCAAGCATTCCCTATGGAGAGATCCACATGGTGAGAAACTGAAGCCT  442

Qy      84  -CTGCCAACCACTGCACTAACCTGCTGGGTCTGAGACTGAGCCACTTTGGAAGCTGATC  142
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      443  CCTACCAAGAGCCAGCACCAACTTGCCAGCTATGTGAATGAGCCATCTTAGAAGTGGGT  502

Qy     143  TTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCACAGCCAACAACAAGACTGCAACC  202
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     503  CTCTAGCCCTAGTCAGGCCTTCATATGACTGCAGCCAGGGCTGATATTTTGACTACAACC  562

Qy     203  TCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATTGCTCCTTGATTCTTAACCCACA  262
```



```

      || || | || | ||||| || | || |||| | |||| | || | ||
Db      563 TCATGAGAGA--CTGAGCCACAACAACCTAGCTAAGAAGCTCCTGAATTCCTACCAACA 620

Qy      263 GAAATTGTGTAAGA 276
      |||| | ||| |||
Db      621 GAAACTATGTGAGA 634
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Search completed: May 31, 2009, 22:28:46
Job time : 1103 secs

SCORE 3.0